

### The I.M.A.G.E. Consortium

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Founded with Drs. Auffray (CNRS) and Polymeropoulos (NCHGR) after discussions at a previous DOE Contractor's- Grantee meeting, the I.M.A.G.E. Consortium is a collaborative effort to systematically identify the majority of genes through the use of arrayed cDNA libraries. Sequence, map, and expression data derived from the clones in these libraries is placed in public databases, and the clones themselves are available royalty-free. Over 200,000 clones have been arrayed at LLNL from 22 human cDNA libraries, and over 200,000 associated EST sequences have been deposited in dbEST primarily through the efforts of the WashU-Merck collaboration. Five organizations worldwide now distribute I.M.A.G.E. clones and associated reagents (such as high-density hybridization filters). In conjunction with efforts such as the Merck Gene Index to determine the number of distinct genes represented (currently over 30,000), I.M.A.G.E. clones are substrates for genome wide transcriptional mapping and full-insert sequencing to complement high-throughput genomic sequencing. We are also conducting subtraction experiments to enrich for clones representing remaining undiscovered genes. Large-scale characterization of arrayed cDNAs from other species is also likely to enhance our knowledge not only of gene number but, more importantly, of both gene diversity and function. For further information, contact the Consortium by e-mail (info@image.llnl.gov) or through the WWW (<http://www-bio.llnl.gov/bbrp/image/image.html>).

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